

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

Claim 1. (Original) A set of oligonucleotide probes, wherein said set comprises at least 10 different oligonucleotides, wherein each oligonucleotide is selected from:

an oligonucleotide having a sequence as set forth in SEQ
ID No. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,
15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28,
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468, 471, 472, 473, 474, 475, 476, 480, 481, 482, 484,
487, 489, 490, 496, 497, 498, 499, 500 or 501,

or an oligonucleotide ~~derived from~~ fragment of said sequence, which fragment is at least 15 bases in length, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide which hybridizes under conditions of high stringency to any of said aforementioned oligonucleotides.

Claim 2. (Currently Amended) A set of oligonucleotide probes as claimed in claim 1, wherein said oligonucleotide probes are each selected from:

an oligonucleotide having a sequence as set forth in SEQ

ID No. 1, 2, 3, 4, 5, 11, 12, 13, 19, 25, 31, 32, 33,
34, 36, 37, 39, 45, 46, 47, 48, 50, 55, 56, 60, 61, 64,
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116, 117, 119, 120, 121, 122, 123, 124, 125, 127, 128,
130, 131, 132, 133, 135, 136, 137, 138, 144, 145, 146,
147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157,
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478, 479, 480, 481, 482, 484, 487, 489, 490, 496, 497,
498, 499 or 501,

or an oligonucleotide ~~derived from~~ fragment of said sequence,
which fragment is at least 15 bases in length, or an
oligonucleotide with a complementary sequence, or a
functionally equivalent oligonucleotide which hybridizes under
conditions of high stringency to any of said aforementioned
oligonucleotides.

Claim 3. (Currently Amended) A set of oligonucleotide
probes as claimed in claim 1, wherein said oligonucleotide
probes are each selected from:

an oligonucleotide having a sequence as set forth in SEQ
ID No. 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,
19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32,
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113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123,
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168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178,
179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189,
190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200,
201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211,
212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222,
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468, 471, 472, 473, 474, 475, 480, 481, 482, 483, 484,
485, 486, 487, 488, 491, 492, 493, 494, 495, 496, 500 or
501,

or an oligonucleotide ~~derived from~~fragment of said sequence,
which fragment is at least 15 bases in length, or an
oligonucleotide with a complementary sequence, or a
functionally equivalent oligonucleotide which hybridizes under
conditions of high stringency to any of said aforementioned
oligonucleotides.

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Claim 4. (Currently Amended) A set of oligonucleotide probes as claimed in ~~any one of claims~~ claim 1 to 3, wherein each probe in said set binds to a different transcript.

Claim 5. (Currently Amended) A set as claimed in ~~any one of claims~~ claim 1 to 4, wherein said set ~~consistsing~~ of from 10 to 500 oligonucleotide probes.

Claims 6-8. (Cancelled).

Claim 9. (Currently Amended) A set of oligonucleotide probes as claimed in ~~any one of claims~~ claim 1 to 5, 7 or 8 or an oligonucleotide probe as claimed in any one of claims 6 to 8, wherein said probes are immobilized on one or more solid supports.

Claims 10-12. (Cancelled).

Claim 13. (Currently Amended) A kit comprising a set of oligonucleotide probes as claimed in claim 1 immobilized on one or more solid supports ~~as defined in claim 9 or 10~~.

Claims 14-15. (Cancelled).

Claim 16. (Currently Amended) ~~The use of a set of probes as described in any one of claims 1 to 5 or 7 to 10 or a kit as described in any one of claims 13 to 15~~ A method for ~~determininge~~ determining the gene expression pattern of a cell ~~pattern reflects the level of gene expression of genes to which said oligonucleotide probes bind,~~ comprising at least the steps of:

- a) isolating mRNA from said cell, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides ~~or a kit~~ probes as defined in ~~any one of claims~~ claim 1 to 5, 7 to 10 or 13 to 15; and
- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern.

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Claim 17. (Currently Amended) A method of preparing a standard gene transcript pattern characteristic of a disease or condition or stage thereof in an organism comprising at least the steps of:

- a) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides probes ~~or a kit~~ as defined in ~~any one of claims~~ claim 1 to 5, 7 to 10 or 13 to 15 specific for said disease or condition or stage thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation; and
- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said ~~oligonucleotides~~ oligonucleotide probes bind, in the sample with the disease, condition or stage thereof.

Claim 18. (Currently Amended) A method of preparing a test gene transcript pattern comprising at least the steps of:

- a) isolating mRNA from the cells of a sample of said test organism, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides probes ~~or a kit~~ as defined in ~~any one of claims~~ claim 1 to 5, 7 to 10 or 13 to 15 specific for a disease or condition or stage thereof in an organism and sample thereof corresponding to

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the organism and sample thereof under investigation; and

- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce said pattern, which reflects ~~reflecting~~ the level of gene expression of genes to which said oligonucleotides probes bind, in said ~~test~~ sample.

Claim 19. (Currently Amended) A method of diagnosing or identifying or monitoring a disease or condition or stage thereof in an organism, comprising the steps of:

- a) isolating mRNA from the cells of a sample of said organism, which may optionally be reverse transcribed to cDNA;
- b) hybridizing the mRNA or cDNA of step (a) to a set of oligonucleotides probes ~~or a kit as defined in any one of claims~~ claim 1 to 5, 7 to 10 or 13 to 15 specific for said disease or condition thereof in an organism and sample thereof corresponding to the organism and sample thereof under investigation;
- c) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides probes bind in said sample; and

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- d) comparing said pattern to a standard diagnostic pattern prepared by
- i) isolating mRNA from the cells of a sample of one or more organisms having the disease or condition or stage thereof, which may optionally be reverse transcribed to cDNA;
 - ii) hybridizing the mRNA or cDNA of step i) to said set of oligonucleotides probes; and
 - iii) assessing the amount of mRNA or cDNA hybridizing to each of said probes to produce a characteristic pattern reflecting the level of gene expression of genes to which said oligonucleotides bind, in the sample with the disease, condition or stage thereof as described in claim 17, using a wherein the sample is from an organism corresponding to the organism and sample under investigation, to thereby determine the degree of correlation indicative of the presence of said disease or condition or a stage thereof in the organism under investigation.

Claims 20-21. (Cancelled).

Claim 22. (Currently Amended) A method as claimed in ~~any one of claims~~ claim 17 to 21, wherein said probes are oligonucleotide probes selected from:

an oligonucleotide having a sequence as set forth in SEQ

ID No. 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,
19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32,
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89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101,
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190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200,
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468, 471, 472, 473, 474, 475, 480, 481, 482, 483, 484,
485, 486, 487, 488, 491, 492, 493, 494, 495, 496, 500 or
501,

or an oligonucleotide fragment of said sequence, which
fragment is at least 15 bases in length, or an oligonucleotide
with a complementary sequence, or a functionally equivalent
oligonucleotide which hybridizes under conditions of high

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stringency to any of said aforementioned oligonucleotides—as defined in claim 3 and said disease is Alzheimer's disease.

Claim 23. (Currently Amended) A method as claimed in ~~any one of claims~~ claim 17 to 21, wherein said probes are oligonucleotide probes selected from:

an oligonucleotide having a sequence as set forth in SEQ

ID No. 1, 2, 3, 4, 5, 11, 12, 13, 19, 25, 31, 32, 33, 34, 36, 37, 39, 45, 46, 47, 48, 50, 55, 56, 60, 61, 64, 66, 68, 73, 74, 75, 76, 77, 78, 80, 83, 85, 86, 90, 96, 98, 99, 100, 101, 105, 106, 107, 109, 111, 114, 115, 116, 117, 119, 120, 121, 122, 123, 124, 125, 127, 128, 130, 131, 132, 133, 135, 136, 137, 138, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 161, 162, 163, 164, 165, 166, 168, 169, 171, 173, 174, 175, 176, 177, 178, 179, 180, 182, 183, 185, 186, 187, 190, 191, 195, 197, 198, 199, 200, 202, 204, 206, 207, 210, 212, 214, 216, 217, 218, 219, 220, 221, 222, 224, 225, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 243, 244, 245, 249, 251, 256, 258, 259, 260, 261, 262, 267, 268, 270, 272, 273, 274, 275, 276, 278, 279, 280, 282, 284, 286, 287, 289, 291, 292, 295, 296, 297, 298, 299, 301, 303, 305, 307, 308, 309, 310, 311, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 351, 352, 353, 355, 356, 357, 359, 361, 363, 364, 365, 366, 367, 368, 369, 370, 371, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 457, 458, 459, 460, 461, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 484, 487, 489, 490, 496, 497, 498, 499 or 501,

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or an oligonucleotide fragment of said sequence, which fragment is at least 15 bases to length, or an oligonucleotide with a complementary sequence, or a functionally equivalent oligonucleotide which hybridizes under conditions of high stringency to any of said aforementioned oligonucleotides—~~as defined in claim 2~~ and said disease is breast cancer.

Claims 24-27. (Cancelled).

Claim 28. (Currently Amended) A method as claimed in ~~any one of claims~~claim 17 to 27, wherein said pattern is expressed as an array of numbers relating to the expression level associated with each probe.

Claim 29. (Currently Amended) A method as claimed in ~~any one of claims~~claim 17 to 28, wherein said organism is a eukaryotic organism, preferably a mammal.

Claim 30. (Original) A method as claimed in claim 29 wherein said organism is a human.

Claim 31. (Cancelled).

Claim 32. (Currently Amended) A method as claimed in ~~any one of claims~~claim 17 to 31, wherein said disease is cancer or a degenerative brain disorder.

Claim 33. (Currently Amended) A method as claimed in ~~any one of claims~~claim 17 to 32, wherein said sample is tissue, body fluid or body waste.

Claim 34. (Currently Amended) A method as claimed in ~~any one of claims~~claim 17 to 33, wherein said sample is peripheral blood.

Claim 35. (Currently Amended) A method as claimed in ~~any one of claims~~claim 17 to 34, wherein the cells in the sample are not disease cells, have not been in contact with such cells and do not originate from the site of the disease or condition.

Claims 36-37. (Cancelled)